

Visualization and Analysis of the Geographic Distribution of Foodborne Disease in Maryland, USA.

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Most foodborne disease cases occur sporadically and are difficult to link to each other or to a source. Geographic information systems (GIS) provide powerful tools for visualizing cases in the context of population density and other spatial features. Cases can be examined for links in space and time and for spatial correspondence with water and other potential risk factors. We developed a georeferenced database from 3341 bacterial foodborne disease cases in the 2001/2002 Maryland FoodNet dataset. These cases represented a catchment area of 7 contiguous counties and Baltimore City. Cases were predominately *Salmonella* but also included *Campylobacter*, *Cryptosporidia*, *E. coli*, *Listeria*, *Shigella*, *Vibrio* and *Yersinia*. Location and case attributes were incorporated into an existing GIS with extensive environmental, hydrologic, landuse, and census data. For a subset of 98 *Salmonella* cases, we appended antimicrobial sensitivity data. A human population density surface was computed using 2000 US Census data (STF 1) and cases were mapped on this surface. Statistical cluster detection methods (spatiotemporal scan statistic and global weighted k-function analysis) were applied for individual pathogens and to assess clustering of resistant isolates among *Salmonella* cases with antimicrobial sensitivities. Case distribution generally followed population distribution; however, case clusters were noted for several pathogens. Resistant isolates were not significantly clustered among the subset of *Salmonella* cases. Consideration of spatial aspects of surveillance data enhances health monitoring and allows more in-depth analyses to uncover risk factors and develop interventions. GIS enables epidemiologists to move from visual to quantitative assessment of patterns and risk factors.